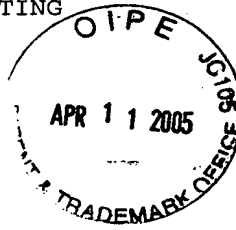


# SEQUENCE LISTING



## (1) GENERAL INFORMATION:

- (i) APPLICANT: Oon, Chong Jin  
Lim, Gek Keow  
Leong, Ai Lin  
Zhao, Yi  
Chen, Wei Ning
- (ii) TITLE OF INVENTION: A VACCINE-INDUCED HEPATITIS B VIRAL STRAIN AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Ladas & Parry
  - (B) STREET: 26 West 61 Street
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10023
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/719,533
  - (B) FILING DATE: 13-DEC-2000
  - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/SG98/00045
  - (B) FILING DATE: 19-JUN-1998
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Mass, Clifford J.
  - (B) REGISTRATION NUMBER: 30,086
  - (C) REFERENCE/DOCKET NUMBER: U-013108-9
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (212) 708-1890

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCACCACT TTCCACCAAA CTCTTCAAGA TCCCAGAGTC AGGGCCCTGT ACTTTCCTGC	60
TGGTGGCTCC AGTTCAGGAA CAGTGAGCCC TGCTCAGAAT ACTGTCTCTG CCATATCGTC	120

AATCTTATCG	AAGACTGGGG	ACCCTGTACC	GAACATGGAG	AACATCGCAT	CAGGACTCCT	180
AGGACCCCTG	CTCGTGTTAC	AGGCGGGGTT	TTTCTTGTTG	ACAAAAATCC	TCACAATACC	240
GCAGAGTCTA	GACTCGTGGT	GGA CT TCTCT	CAATTTTCTA	GGGGGAACAC	CCGTGTGTCT	300
TGGCCAAAAT	TCGCAGTCCC	AAATCTCCAG	TCACTCACCA	ACCTGTTGTC	CTCCAATTTG	360
TCCTGGTTAT	CGCTGGATGT	GTCTGCGGCG	TTTTATCATC	TTCCTCTGCA	TCCTGCTGCT	420
ATGCCTCATC	TTCTTGTTGG	TTCTTCTGGA	CTATCAAGGT	ATGTTGCCCG	TTTGTCTCT	480
AATTCCAGGA	TCAACAACAA	CCAGCACC GG	ACCATGCAAA	ACCTGCACAA	CTCCTGCTCA	540
AGGAACCTCT	ATGTTTCCCT	CATGTTGCTG	TACAAAACCT	ACGGACAGAA	ACTGCACCTG	600
TATTCCCATC	CCATCATCTT	GGGCTTTCGC	AAAATACCTA	TGGGAGTGGG	CCTCAGTCCG	660
TTTCTCTTGG	CTCAGTTTAC	TAGTGCCATT	TGTT CAGTGG	TTCGTAGGGC	TTTCCCCCAC	720
TGTCTGGCTT	TCAGTTATAT	GGATGATGTG	GTTTTGGGGG	CCAAGTCTGT	ACAACATCTT	780
GAGTCCCTTT	ATGCCGCTGT	TACCAATTTT	CTTTTGTCTT	TGGGTATACA	TTTAAACCCT	840
CACAAAACAA	AAAGATGGGG	ATATTCCCTT	AACTTCATGG	GATATGTCAT	TGGGAGTTGG	900
GGCACATTGC	CACAGGAACA	TATTGTACAA	AAAATCAAAA	TGTGTTTTAG	GAAACTTCCT	960
GTAAACAGGC	CTATTGATTG	GAAAGTATGT	CAACGAATTG	TGGGTCTTTT	GGGGTTTGCC	1020
GGCCCTTTCA	CGCAATGTGG	ATATCCTGCT	TTAATGCCTT	TATATGCATG	TATACAAGCA	1080
AAACAGGCTT	TTACTTTCTC	GCAAACCTTAC	AAGACCTTTC	TAAGTAAACA	GTATCTGAAC	1140
CTTTACCCCG	TTGCTCGGCA	ACGCCCTGGT	CTGTGCCAAG	TGTTTGCTGA	CGCAACCCCC	1200
ACTGGTTGGG	GCTTGGCCAT	AGGCCATCAG	CGCATGCGTG	GAACCTTTGT	GTCTCCTCTG	1260
CCGATCCATA	CTGCGGAACT	CCTAGCCGCT	TGTTTTGCTC	GCAGCAGGTC	TGGGGCAAAA	1320
CTCATCGGGA	CTGACAATTC	TGTCGTGCTC	TCCCGCAAGT	ATACATCATT	TCCATGGCTG	1380
CTAGGCTGTG	CTGCCAACTG	GATCCTGCGC	GGGACGTCCT	TTGTTTACGT	CCCGTCGGCG	1440
CTGAATCCCG	CGGACGACCC	CTCCCGGGGC	CGCTTGGGGC	TCTACCGCCC	GCTTCTCCGC	1500
CTGTTATACC	GACCGACCAC	GGGGCGCACC	TCTCTTTACG	CGGACTCCCC	GTCTGTGCCT	1560
TCTCATCTGC	CGGACCGTGT	GCACTTCGCT	TCACCTCTGC	ACGTCGCATG	GAGACCACCG	1620
TGAACGCCCA	CGGGAACCTG	CCCAAGGTCT	TGCATAAGAG	GACTCTTGGA	CTTTCAGCAA	1680
TGTCAACGAC	CGACCTTGAG	GCATACTTCA	AAGACTGTGT	GTTTAATGAG	TGGGAGGAGT	1740
TGGGGGAGGA	GGTTAGGTTA	AAGGTCTTTG	TACTAGGAGG	CTGTAGGCAT	AAATTGGTGT	1800
GTTCAACATC	ACCATGCAAC	TTTTTCACCT	CTGCCTAATC	ATCTCATGTT	CATGTCCTAC	1860
TGTTCAAGCC	TCCAAGCTGT	GCCTTGGGTG	GCTTTGGGGC	ATGGACATTG	ACCCGTATAA	1920

AGAATTTGGA GCTTCTGTGG AGTTACTCTC TTTTTTGCCT TCTGACTTTT TTCCTTCTAT	1980
TCGAGATCTC CTCGACACCG CCTCTGCTCT GTATCGGGAG GCCTTAGAGT CTCCGGAACA	2040
TTGTTACCT CACCATACGG CACTCAGGCA AGCTATTCTG AGTTGGGGTG AGTTAATGAA	2100
TCTAGCCACC TGGGTGGGAA GTAATTTGGA AGATCCAGCA TCCAGGGAAT TAGTAGTCAG	2160
CTATGTCAAC GTTAATATGG GCCTAAAAAT CAGACAATA TTGTGGTTTC ACATTTCTCTG	2220
TCTTACTTTT GGGAGAGAAA CTGTTCTTGA ATATTTGGTG TCTTTTGGAG TGTGGATTCTG	2280
CACTCCTCCT GCATATAGAC CACCAAATGC CCCTATCTTA TCAACACTTC CGGAAACTAC	2340
TGTTGTTAGA CGAAGAGGCA GGTCCCCTAG AAGAAGAACT CCCTCGCCTC GCAGACGAAG	2400
GTCTCAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGGAA TCTCAATGTT AGTATTCCTT	2460
GGACACATAA GGTGGGAAAC TTTACGGGGC TTTATTCTTC TACGGTACCT TGCTTTAATC	2520
CTAAATGGCA AACTCCTTCT TTTCCGGACA TTCATTTGCA GGAGGACATT CTTGATAGAT	2580
GTAAGCAATT TGTGGGGCCC CTTACAGTAA ATGAAAACAG GAGACTAAAA TTAATTATGC	2640
CTGCTAGGTT TTATCCAAAT GTTACTAAAT ATTTGCCCTT AGATAAAGGG ATCAAACCAT	2700
ATTATCCAGA GTATGTAGTT AATCATTACT TCCAGACGCG ACATTATTTA CAACTCTTT	2760
GGAAGGCGGG GATCTTATAT AAAAGAGAGT CCACACGTAG CGCCTCATTT TGCGGGTCAC	2820
CATATTCTTG GGAACAAGAT CTACAGCATG GGAGGTTGGT CTTCCAAACC TCGAAAAGGC	2880
ATGGGGACAA ATCTTTCTGT CCCCAATCCC CTGGGATTCT TCCCCGATCA TCAGTTGGAC	2940
CCTGCATTCA AAGCCAACTC AGAAAATCCA GATTGGGACC TCAACCCGCA CAAGGACAAC	3000
TGGCCGGACG CCAACAAGGT GGGAGTGGGA GCATTGCGGC CAGGGTTCAC CCCTCCTCAT	3060
GGGGGACTGT TGGGGTGGAG CCCTCAGGCT CAGGGCCTAC TCACAACTGT GCCAGCAGCT	3120
CCTCCTCTG CCTCCACCAA TCGGCAGTCA GGAAGGCAGC CTACTCCCTT ATCTCCACCT	3180
CTAAGGGACA CTCATCCTCA GGCCATGCAG TGGAA	3215

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 843 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Leu	Ser	Tyr	Gln	His	Phe	Arg	Lys	Leu	Leu	Leu	Leu	Asp	Glu
1				5					10					15	

Glu	Ala	Gly	Pro	Leu	Glu	Glu	Glu	Leu	Pro	Arg	Leu	Ala	Asp	Glu	Gly
			20					25					30		
Leu	Asn	Arg	Arg	Val	Ala	Glu	Asp	Leu	Asn	Leu	Gly	Asn	Leu	Asn	Val
		35					40					45			
Ser	Ile	Pro	Trp	Thr	His	Lys	Val	Gly	Asn	Phe	Thr	Gly	Leu	Tyr	Ser
	50					55					60				
Ser	Thr	Val	Pro	Cys	Phe	Asn	Pro	Lys	Trp	Gln	Thr	Pro	Ser	Phe	Pro
65				70						75					80
Asp	Ile	His	Leu	Gln	Glu	Asp	Ile	Leu	Asp	Arg	Cys	Lys	Gln	Phe	Val
				85					90					95	
Glu	Pro	Leu	Thr	Val	Asn	Glu	Asn	Arg	Arg	Leu	Lys	Leu	Ile	Met	Pro
			100					105					110		
Ala	Arg	Phe	Tyr	Pro	Asn	Val	Thr	Lys	Tyr	Leu	Pro	Leu	Asp	Lys	Gly
		115					120					125			
Ile	Lys	Pro	Tyr	Tyr	Pro	Glu	Tyr	Val	Val	Asn	His	Tyr	Phe	Gln	Thr
	130					135					140				
Arg	His	Tyr	Leu	His	Thr	Leu	Trp	Lys	Ala	Gly	Ile	Leu	Tyr	Lys	Arg
145					150					155					160
Glu	Ser	Thr	Arg	Ser	Ala	Ser	Phe	Cys	Gly	Ser	Pro	Tyr	Ser	Trp	Glu
				165					170					175	
Gln	Asp	Leu	Gln	His	Gly	Arg	Leu	Val	Phe	Gln	Thr	Ser	Lys	Arg	His
			180					185					190		
Gly	Asp	Lys	Ser	Phe	Cys	Pro	Glu	Ser	Pro	Gly	Ile	Leu	Pro	Arg	Ser
		195					200					205			
Ser	Val	Gly	Pro	Cys	Ile	Gln	Ser	Gln	Leu	Arg	Lys	Ser	Arg	Leu	Gly
	210					215					220				
Pro	Gln	Pro	Ala	Gln	Gly	Gln	Leu	Ala	Gly	Arg	Gln	Gln	Gly	Gly	Ser
225				230						235					240
Gly	Ser	Ile	Arg	Ala	Arg	Val	His	Pro	Ser	Ser	Trp	Gly	Thr	Val	Gly
				245					250					255	
Val	Glu	Pro	Ser	Gly	Ser	Gly	Pro	Thr	His	Asn	Cys	Ala	Ser	Ser	Ser
			260					265					270		
Ser	Ser	Cys	Leu	His	Gln	Ser	Ala	Val	Arg	Lys	Ala	Ala	Tyr	Ser	Leu
		275					280					285			
Ile	Ser	Thr	Ser	Lys	Gly	His	Ser	Ser	Ser	Gly	His	Ala	Val	Glu	Leu
	290					295					300				
His	His	Phe	Pro	Pro	Asn	Ser	Ser	Arg	Ser	Gln	Ser	Gln	Gly	Pro	Val
305					310					315					320
Leu	Ser	Cys	Trp	Trp	Leu	Gln	Phe	Arg	Asn	Ser	Glu	Pro	Cys	Ser	Glu
				325					330					335	

Tyr Cys Leu Cys His Ile Val Asn Leu Ile Glu Asp Trp Gly Pro Cys  
 340 345 350  
 Thr Glu His Gly Glu His Arg Ile Arg Thr Pro Arg Thr Pro Ala Arg  
 355 360 365  
 Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala  
 370 375 380  
 Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Thr  
 385 390 395 400  
 Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr  
 405 410 415  
 Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala  
 420 425 430  
 Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu  
 435 440 445  
 Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn  
 450 455 460  
 Ser Arg Ile Asn Asn Asn Glu His Arg Thr Met Glu Asn Leu His Asn  
 465 470 475 480  
 Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys Thr  
 485 490 495  
 Tyr Gly Gln Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe  
 500 505 510  
 Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln  
 515 520 525  
 Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys  
 530 535 540  
 Leu Ala Phe Ser Tyr Met Asp Asp Val Val Leu Gly Ala Lys Ser Val  
 545 550 555 560  
 Gln His Leu Glu Ser Leu Tyr Ala Ala Val Thr Asn Phe Leu Leu Ser  
 565 570 575  
 Leu Gly Ile His Leu Asn Pro His Lys Thr Lys Arg Trp Gly Tyr Ser  
 580 585 590  
 Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln  
 595 600 605  
 Glu His Ile Val Gln Lys Ile Lys Met Cys Phe Arg Lys Leu Pro Val  
 610 615 620  
 Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu  
 625 630 635 640  
 Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro  
 645 650 655

Leu	Tyr	Ala	Cys	Ile	Gln	Ala	Lys	Gln	Ala	Phe	Thr	Phe	Ser	Gln	Thr	660	665	670
Tyr	Lys	Thr	Phe	Leu	Ser	Lys	Gln	Tyr	Leu	Asn	Leu	Tyr	Pro	Val	Ala	675	680	685
Arg	Gln	Arg	Pro	Gly	Leu	Cys	Glu	Val	Phe	Ala	Asp	Ala	Thr	Pro	Thr	690	695	700
Gly	Trp	Gly	Leu	Ala	Ile	Gly	His	Gln	Arg	Met	Arg	Gly	Thr	Phe	Val	705	710	715
Ser	Pro	Leu	Pro	Ile	His	Thr	Ala	Glu	Leu	Leu	Ala	Ala	Cys	Phe	Ala	725	730	735
Arg	Ser	Arg	Ser	Gly	Ala	Lys	Leu	Ile	Gly	Thr	Asp	Asn	Ser	Val	Val	740	745	750
Leu	Ser	Arg	Lys	Tyr	Thr	Ser	Phe	Pro	Trp	Leu	Leu	Gly	Cys	Ala	Ala	755	760	765
Asn	Trp	Ile	Leu	Arg	Gly	Thr	Ser	Phe	Val	Tyr	Val	Pro	Ser	Ala	Leu	770	775	780
Asn	Pro	Ala	Asp	Asp	Pro	Ser	Arg	Gly	Arg	Leu	Gly	Leu	Tyr	Arg	Pro	785	790	795
Leu	Leu	Arg	Leu	Leu	Tyr	Arg	Pro	Thr	Thr	Gly	Arg	Thr	Ser	Leu	Tyr	805	810	815
Ala	Asp	Ser	Pro	Ser	Val	Pro	Ser	His	Leu	Pro	Asp	Arg	Val	His	Phe	820	825	830
Ala	Ser	Pro	Leu	His	Val	Ala	Trp	Arg	Pro	Pro						835	840	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Lys	Ala	Asn	Ser	Glu	Asn	Pro	Asp	Trp	Asp	Leu	Asn	Pro	His	35	40	45	

Lys	Asp	Asn	Trp	Pro	Asp	Ala	Asn	Lys	Val	Gly	Val	Gly	Ala	Phe	Gly		
50						55					60						
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln		
65					70					75					80		
Ala	Gln	Gly	Leu	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser		
				85					90					95			
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Leu	Ser	Pro	Pro	Leu		
			100					105					110				
Arg	Asp	Thr	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His		
		115					120					125					
Gln	Thr	Leu	Gln	Asp	Pro	Arg	Val	Arg	Ala	Leu	Tyr	Phe	Pro	Ala	Gly		
	130					135					140						
Gly	Ser	Ser	Ser	Gly	Thr	Val	Ser	Pro	Ala	Gln	Asn	Thr	Val	Ser	Ala		
145					150					155					160		
Ile	Ser	Ser	Ile	Leu	Ser	Lys	Thr	Gly	Asp	Pro	Val	Pro	Asn	Met	Glu		
				165					170					175			
Asn	Ile	Ala	Ser	Gly	Leu	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly		
			180					185					190				
Phe	Phe	Leu	Leu	Thr	Lys	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser		
		195					200					205					
Trp	Trp	Thr	Ser	Leu	Asn	Phe	Leu	Gly	Gly	Thr	Pro	Val	Cys	Leu	Gly		
	210					215					220						
Gln	Asn	Ser	Gln	Ser	Gln	Ile	Ser	Ser	His	Ser	Pro	Thr	Cys	Cys	Pro		
225					230					235					240		
Pro	Ile	Cys	Pro	Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile		
				245					250					255			
Phe	Leu	Cys	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu		
			260					265					270				
Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Thr		
		275					280					285					
Thr	Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys	Thr	Thr	Pro	Ala	Gln	Gly		
	290					295					300						
Thr	Ser	Met	Phe	Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Thr	Asp	Arg	Asn		
305					310					315					320		
Cys	Thr	Cys	Ile	Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Lys	Tyr	Leu		
				325					330					335			
Trp	Glu	Trp	Ala	Ser	Val	Arg	Phe	Ser	Trp	Leu	Ser	Leu	Leu	Val	Pro		
			340					345					350				
Phe	Val	Gln	Trp	Phe	Val	Gly	Leu	Ser	Pro	Thr	Val	Trp	Leu	Ser	Val		
		355					360					365					





(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Ala	Arg	Leu	Cys	Cys	Gln	Leu	Asp	Pro	Ala	Arg	Asp	Val	Leu	
1				5					10					15		
Cys	Leu	Arg	Pro	Val	Gly	Ala	Glu	Ser	Arg	Gly	Arg	Pro	Leu	Pro	Gly	
			20					25					30			
Pro	Leu	Gly	Ala	Leu	Pro	Pro	Ala	Ser	Pro	Pro	Val	Ile	Pro	Thr	Asp	
		35					40					45				
His	Gly	Ala	His	Leu	Ser	Leu	Arg	Gly	Leu	Pro	Val	Cys	Ala	Phe	Ser	
	50					55					60					
Ser	Ala	Gly	Pro	Cys	Ala	Leu	Arg	Phe	Thr	Ser	Ala	Arg	Arg	Met	Glu	
65					70					75					80	
Thr	Thr	Val	Asn	Ala	His	Gly	Asn	Leu	Pro	Lys	Val	Leu	His	Lys	Arg	
			85						90					95		
Thr	Leu	Gly	Leu	Ser	Ala	Met	Ser	Thr	Thr	Asp	Leu	Glu	Ala	Tyr	Phe	
			100					105					110			
Lys	Asp	Cys	Val	Phe	Asn	Glu	Trp	Glu	Glu	Leu	Gly	Glu	Glu	Val	Arg	
		115					120					125				
Leu	Lys	Val	Phe	Val	Leu	Gly	Gly	Cys	Arg	His	Lys	Leu	Val	Cys	Ser	
		130				135					140					
Pro	Ser	Pro	Cys	Asn	Phe	Phe	Thr	Ser	Ala							
145					150											

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAAGCTTATG CCCCTATCTT ATCAACACTT CCGGA

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTCTAGAC TCTGCGGTAT TGTGA

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCTAGAC TCGTGGTGGA CTTCT

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAATTCT CACGGTGGTC TCCATGCGAC GT

32

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGTTTACG TCCCGT

16

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAAGCTTAG TTTCCGGAAG TGTTGAT